

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/559,097
Source: IFWP
Date Processed by STIC: 12/14/2005

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IFWP

RAW SEQUENCE LISTING

DATE: 12/14/2005

PATENT APPLICATION: US/10/559,097

TIME: 14:59:33

Input Set : A:\053584txt.TXT

Output Set: N:\CRF4\12142005\J559097.raw

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3 <110> APPLICANT: CropDesign N.V.
5 <120> TITLE OF INVENTION: Monocotyledonous plants having improved growth
characteristics
6     and a method for making the same
8 <130> FILE REFERENCE: CD-097-PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/559,097
C--> 10 <141> CURRENT FILING DATE: 2005-12-01
10 <150> PRIOR APPLICATION NUMBER: EP 03076719.8
11 <151> PRIOR FILING DATE: 2003-06-03
13 <160> NUMBER OF SEQ ID NOS: 30
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2313
19 <212> TYPE: DNA
20 <213> ORGANISM: Oryza sativa
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25 tctgogaatc gaattctttg tttttttttc tctaatttta cggggaattg tcgaattagg      180
26 cattcaccaa cgagcaagag gggagtggat tggttggtta aagctccgca tcttgcgggc      240
27 gaaatctcgc tctcttctct gcggtgggtg gccggagaag tcgccgccgg tgaggcatgg      300
28 ggatggagggt ggcggcgggc cggctggggg ctctgtacac gacctccgac tacgcgtcgg      360
29 tgggtgtccat caacctgttc gtcgcgtcgc tctgcgcctg catcgtcctc ggccacctcc      420
30 tcgaggagaa tcgctgggtc aatgagtcca tcaccgcgct catcatcggg ctctgcaccg      480
31 gcgtggtgat cttgctgatg accaaagga agagctcgca cttattcgtc ttcagtgagg      540
32 atctcttctt catctacctc ctccctccga tcattctcaa tgcaggtttt caggtaaaga      600
33 aaaagcaatt ctcccggaat ttcattgacga tcacattatt tggagccgtc gggacaatga      660
34 tatecttttt cacaatatct attgctgcc a ttgcaatatt cagcagaatg aacattggaa      720
35 cgctggatgt aggagatttt cttgcaattg gagccatctt ttctgcgaca gattctgtct      780
36 gcacattgca ggtcctcaat caggatgaga cacccttttt gtacagtctg gtattcgggtg      840
37 aagggtgtgt gaacgatgct acatcaattg tgcttttcaa cgcactacag aactttgatc      900
38 ttgtccacat agatgcggct gtcgttctga aattcttggg gaacttcttt tatttatatt      960
39 tgtcgagcac cttccttggg gtatttgctg gattgctcag tgcatacata atcaagaagc     1020
40 tatacattgg aaggcattct actgaccgtg aggttgcctt tatgatgctc atggcttacc     1080
41 tttcatatat gctggctgag ttgctagatt tgagcggcat tctcaccgta ttcttctgtg     1140
42 gtattgtaat gtcacattac acttggcata acgtcacaga gagttcaaga gttacaacaa     1200
43 agcacgcatt tgcaactctg tcttctcatt ctgagacttt tctcttctctg tatgttgagg     1260
44 tggatgcatt ggatattgaa aaatgggagt ttgccagtga cagacctggc aaatccattg     1320
45 ggataagctc aattttgcta ggattgggtc tgattggaag agctgctttt gtattcccgc     1380
46 tgtcgttctt gtcgaacctc acaaagaagg caccgaatga aaaaataacc tggagacagc     1440
47 aagttgtaat atggtgggct gggctgatga gaggagctgt gtcgattgct cttgcttaca     1500
48 ataagtttac aagatctggc catactcagc tgcacggcaa tgcaataatg atcaccagca     1560
49 ccatcactgt cgttcttttt agcactatgg tatttgggat gatgacaaag ccattgatca     1620
50 ggctgctgct accggcctca ggccatcctg tcacctctga gccttcatca ccaaagtccc     1680

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51 tgcattctcc tctcctgaca agcatgcaag gttctgacct cgagagtaca accaacattg 1740
52 tgaggccttc cagcctccgg atgctcctca ccaagccgac ccacactgtc cactactact 1800
53 ggcgcaagtt cgacgacgcg ctgatgcgac cgatgtttgg cgggcgcggg ttcgtgccct 1860
54 tctcccctgg atcaccaacc gagcagagcc atggaggaag atgaacagtg caaagaaatg 1920
55 agaatggaat ggttgatgag gagaatacat gtaaaatgtg acagcaaaag agagaaggca 1980
56 agttttgggt ttgtagagtt tggtgctgc taatgagttg ttgatagtgc ctatattctt 2040
57 cagaacttca gatggtgcct caccaaggcc taagagccag gaggaccttc tgataatggt 2100
58 tcgggatgat tggtttgttc tgtcaggatg aaccctagtg agtgacacag ggtgatgtgc 2160
59 tccgacaacc tgtaaatttt gtagattaac agccccattt gtacctgtct accatcttta 2220
60 gttggcgggt gttctttcct agttgccacc ctgcatgtaa aatgaaattc tccgccaaaa 2280
61 tagatttgtg tgtataataa ttttgcttgg ttg 2313

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63 <210> SEQ ID NO: 2

64 <211> LENGTH: 535

65 <212> TYPE: PRT

66 <213> ORGANISM: Oryza sativa

68 <400> SEQUENCE: 2

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70 1 5 10 15
72 Ser Asp Tyr Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Leu
73 20 25 30
75 Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val
76 35 40 45
78 Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val
79 50 55 60
81 Ile Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser
82 65 70 75 80
84 Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
85 85 90 95
87 Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile
88 100 105 110
90 Thr Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser
91 115 120 125
93 Ile Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp
94 130 135 140
96 Val Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser
97 145 150 155 160
99 Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Phe Leu Tyr
100 165 170 175
102 Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val
103 180 185 190
105 Leu Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala
106 195 200 205
108 Val Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser
109 210 215 220
111 Thr Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys
112 225 230 235 240
114 Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met
115 245 250 255
117 Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu

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118          260          265          270
120 Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr
121          275          280          285
123 Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala
124          290          295          300
126 Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val
127 305          310          315          320
129 Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg
130          325          330          335
132 Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu
133          340          345          350
135 Ile Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu
136          355          360          365
138 Thr Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val
139          370          375          380
141 Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala
142 385          390          395          400
144 Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala
145          405          410          415
147 Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val
148          420          425          430
150 Phe Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser
151          435          440          445
153 Gly His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser
154          450          455          460
156 Pro Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn
157 465          470          475          480
159 Ile Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His
160          485          490          495
162 Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro
163          500          505          510
165 Met Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr
166          515          520          525
168 Glu Gln Ser His Gly Gly Arg
169          530          535

171 <210> SEQ ID NO: 3
172 <211> LENGTH: 1614
173 <212> TYPE: DNA
174 <213> ORGANISM: Arabidopsis thaliana
176 <400> SEQUENCE: 3
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178 gttgcgttga atctctttgt tgcacttctt tgtgcttgta ttgttcttgg tcatcttttg      120
179 gaagagaata gatggatgaa cgaatccatc accgccttgt tgattgggct aggcactggt      180
180 gttaccattt tgttgattag taaaggaaaa agctcgcac tctcgtctt tagtgaagat      240
181 cttttcttca tatatctttt gccacccatt atattcaatg cagggtttca agtaaaaaag      300
182 aagcagtttt tccgcaattt cgtgactatt atgctttttg gtgctgttgg gactattatt      360
183 tcttgcacaa tcatatctct aggtgtaaca cagttcttta agaagttgga cattggaacc      420
184 tttgacttgg gtgattatct tgctattggg gccatatttg ctgcaacaga ttcagtatgt      480
185 aactgcagg ttctgaatca agacgagaca ctttgccttt acagtcttgt attcggagag      540

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186 ggtgttgatga atgatgcaac gtcagttgtg gtcttcaacg cgattcagag ctttgatctc 600
187 actcacctaa accacgaagc tgcttttcat cttcttgga acttcttgta tttgtttctc 660
188 ctaagtacct tgcttggtgc tgcaaccggg ctgataagtg cgtatgttat caagaagcta 720
189 tactttggaa ggcactcaac tgaccgagag gttgccctta tgatgcttat ggcgtatctt 780
190 tcttatatgc ttgctgagct tttcgacttg agcgggtatcc tcaactgtgtt tttctgtggg 840
191 attgtgatgt cccattacac atggcacaat gtaacggaga gctcaagaat aacaacaaag 900
192 catacctttg caactttgtc atttcttgcg gagacattta ttttcttgta tgttggaatg 960
193 gatgccttgg acattgacaa gtggagatcc gtgagtga caaccgggaac atcgatcgca 1020
194 gtgagctcaa tcctaattgg tctgggtcatg gttggaagag cagcgttcgt ctttccgtta 1080
195 tcgtttctat ctaacttagc caagaagaat caaagcgaga aaatcaactt taacatgcag 1140
196 gttgtgattt ggtggtctgg tctcatgaga ggtgctgtat ctatggctct tgcatacaac 1200
197 aagtttaciaa gggccgggca cacagatgta cgcgggaatg caatcatgat cagcagtagc 1260
198 ataactgtct gtcttttttag cacagtgggtg tttggtagtc tgaccaaacc actcataagc 1320
199 tacctattac cgcaccagaa cgccaccacg agcatgttat ctgatgacaa caccacaaaa 1380
200 tccatacata tccctttggt ggaccaagac tcgttcattg agccttcagg gaaccacaat 1440
201 gtgcctcggc ctgacagtat acgtggcttc ttgacacggc ccactcgaac cgtgcattac 1500
202 tactggagac aatttgatga ctcttcatg cgaccctgtc ttggagggtc tggctttgta 1560
203 ccctttgttc caggttctcc aactgagaga aaccctcctg atcttagtaa ggct 1614

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205 <210> SEQ ID NO: 4

206 <211> LENGTH: 538

207 <212> TYPE: PRT

208 <213> ORGANISM: Arabidopsis thaliana

210 <400> SEQUENCE: 4

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214 His Ala Ser Val Val Ala Leu Asn Leu Phe Val Ala Leu Leu Cys Ala
215 20 25 30
217 Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu
218 35 40 45
220 Ser Ile Thr Ala Leu Leu Ile Gly Leu Gly Thr Gly Val Thr Ile Leu
221 50 55 60
223 Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp
224 65 70 75 80
226 Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe
227 85 90 95
229 Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu
230 100 105 110
232 Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly
233 115 120 125
235 Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly
236 130 135 140
238 Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys
239 145 150 155 160
241 Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu
242 165 170 175
244 Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe
245 180 185 190
247 Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala
248 195 200 205

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250 Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu
251      210      215      220
253 Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu
254 225      230      235      240
256 Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu
257      245      250      255
259 Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly
260      260      265      270
262 Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp
263      275      280      285
265 His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala
266      290      295      300
268 Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met
269 305      310      315      320
271 Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly
272      325      330      335
274 Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly
275      340      345      350
277 Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys
278      355      360      365
280 Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp
281      370      375      380
283 Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn
284 385      390      395      400
286 Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met
287      405      410      415
289 Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly
290      420      425      430
292 Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala
293      435      440      445
295 Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile
296      450      455      460
298 Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn
299 465      470      475      480
301 Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg
302      485      490      495
304 Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro
305      500      505      510
307 Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr
308      515      520      525
310 Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala
311      530      535
313 <210> SEQ ID NO: 5
314 <211> LENGTH: 2232
315 <212> TYPE: DNA
316 <213> ORGANISM: Medicago sativa
318 <400> SEQUENCE: 5
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320 ctctaaatag aatatcgaca gagtgactca acaagattat taggagtgat aatcttccac 120

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date